

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: I.N.S.E.R.M
- (B) STREET: 101, rue de Tolbiac
- (C) CITY: PARIS CEDEX 13
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE (ZIP): 75654

(ii) TITLE OF THE INVENTION: DNA, specific proteins and peptides of the *Neisseria meningitidis* species bacteria, methods for obtaining them and their biological applications.

(iii) NUMBER OF SEQUENCES: 99

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCCGCTGC CGGCAGACGA ATATCAAGAC ATCTTCGATT TTATGAAACA GTATGACTTG 60
 TCTTACCCGT ATGAATATCT GCAGGATTGG ATAGATTACT ATACGTTCAA AACCGATAAG 120
 CTGGTATTTG GTAACGCGAA GCGAGAGTGA GCCGTAAAAC TCTGAGCTCC TGTTTTATAG 180
 ATTACAACCTT TAGGCCGTCT TAAAGCTGAA AGATTTTCGA AAGCTATAAA TTGAAGCCCT 240
 TCCACAGTAC ATAGATC 257

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GATCATGTTC AAATAGATAG GCATGGGAAG CTGCAGCTCT AACGTCCATG AAAATATGTT 60
 GCATAGCTGC AAGCGGAACG CCTTTTCTTT CATCTACATA ATCTATAGAG TCAAGGCAAC 120
 CGCTATTGAA ATTAGCAGTA TTGCCTATGA TTACATTAGT AATATGCTCA TACCATTTTT 180

GGGTGGTCAT CATATTGTGC CCCATTGTGA TCTCCTTATA TTGGTTTTAG AAGGAACTTT 240

GACAGGAAGA ATAACGGCCT TACCTGTTTG ACGATC 276

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATCTGGTGG TGTTTGCACA GGTAGGCGCA TACTTGTTTCG GGACTGAGTT TGCGGCGGAT 60

AAGGGTGTCG ATGTGCTGAA TCAGCTGCGA ATCGAGCTTA TAGGGTTGTC GCTTACGCTG 120

TTTGATAGTC CGGCTTTGCC GCTGGGCTTT TTCGGCGCTG TATTGCTGCC CTTGGGTGCG 180

GTGCCGTCTG ATTTGCGGCG TGATGGTGCT TTTGTGGCGG TTAAGCTGTT TGGCGATTTT 240

GGTGACGGTG CAGTGGCGGG ACAGGTATTG GATGTGGTAT CGTTCGCCTT GGGTCAGTTG 300

CGTGTAGCTC ATGGCAATCT TTCTTGCAAG AAAGGCCGTA TGCTACCGCA TACTGGCCTT 360

TTTCTGTTAG GGAAAGTTGC ACTTCAAATG CGAATCCGCC GACCTCTTTC AGTTACAGCA 420

GCTTGATC 428

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCTGCAT TGACATCGGC CTTGGCTGTC AGGGTATTGT GACCGGTAAA GTCGGCATT A 60
 CCGTTGGCCA ATAAGGATAC ATGACCGTCT GCAGAAACAG CATGAAGGCC GTCTGAAACG 120
 ATATTGCCCT GCAATGCGGT GGTTCGAGA GCCTTGGCTG CGTTCAGCTT GGTATTGCGA 180
 AGCTGAATAT TGCCTTTGGC TGCCTGAATG TGCAGATTAC CCGAGTTGGT ACGCAGATTG 240
 GTATTGGTAA CATTGAGCAA GCCTGCCTCC ACACCCATGT CTTTGGAGGC AGTGAGGGTT 300
 TTA CTGGTGC CGGTAATATG GGCAGCGTTA TCCGATTTC AATGGATGCT GGCCGGCAGA 360
 CAAATCTTTA TCAACATTCA AATTCAGATC 390

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: Z2491

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GATCAGATTG | GTGAAGACGG | TATTACCGTC | AATGTTGCAG | GCCGTTCTGGG | ATATACGGCG | 60 |
| AAAATCGACG | TGTCTCCGAG | TACCGATTTG | GCGGTTTATG | GCCATATTGA | AGTTGTACGG | 120 |
| GGTGCAACGG | GGTTGACCCA | ATCCAATTCA | GAGCCGGGTG | GAACCGTCAA | TTTGATC | 177 |

(A) LENGTH: 341 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: Z2491

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GATCAATGAT | GCTACTATTC | AAGCGGGCAG | TTCCGTGTAC | AGCTCCACCA | AAGGCGATAC | 60 |
| TGAATTGGGT | GAAAATACCC | GTATTATTGC | TGAAAACGTA | ACCGTATTAT | CTAACGGTAG | 120 |
| TATTGGCAGT | GCTGCTGTAA | TTGAGGCTAA | AGACACTGCA | CACATTGAAT | CGGGCAAACC | 180 |
| GCTTTCTTTA | GAAACCTCGA | CCGTTGCCTC | CAACATCCGT | TTGAACAACG | GTAACATTAA | 240 |
| AGGCGGAAAG | CAGCTTGCTT | TACTGGCAGA | CGATAACATT | ACTGCCAAAA | CTACCAATCT | 300 |

GAATACTCCC GGCAATCTGT ATGTTTCATAC AGGTAAAGAT C

341

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

| | | | | | | | | | | | | |
|----------|-----|---------|------|--------|------|--------|------|--------|------|--------|------|-----|
| GATCCAAC | TG | TTTGATT | TTTA | CTGGCT | GCTT | CTCCAT | GCGC | GGTATT | GACC | AAAGCC | GCAA | 60 |
| GGATATT | CGC | TTCCAG | ATTG | TCTTTC | CAGG | TGCCGC | CGGT | GACAGC | GGTA | TTAATC | CAGT | 20 |
| CGGCACT | GCC | CGCATT | GGCT | AGGTTG | ACGG | TCAGGT | TGTT | GATC | | | | 164 |

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATCAATCAC ACATCTTGTC ATTTTTCGA TTCCTTCATT TCGGTTTCTA ATGTTTCAAT 60
 TCTTGCGGCC ATTTCTGAA TGGCTTTAGT CAAAACGGGG ATGAACGCTT CGTATTTCGAC 120
 GGTGTAGGTA TCGTTTGTTC TATTTACCAT CGGCAATCGA CCATATTCAT CTTCCAGCGC 180
 AGCAATGTCC TGGGCAATAA ACCAATGCCG CAACCGATC 219

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTTGGGT AAGCCCCAA CCTGCATAGA AAGGCAGGCC GTAGCAGCTG ACTTTTTTGC 60
 CGCGCAACAA GGCTTCAAAA CCGGTCAGCG AAGTCATGGT ATGTATTTTCG TCTGCGTATT 120
 GGAGACAGGT CAGGATGTCG GCTTGTTTCGG CGGTTTGGTC GGCATATCGT GCAGCATCAT 180
 CAGGGGAAAT ATGGCCGATG CGGTTACCGC TGA CTACATC GGGATGCGGT TTGTAGATGA 240
 TATAGGCATT GGGGTTTCGT TCGCGTACGG TACGGAGCAA ATCCAGATTG CGGTAGATTT 300
 GGGGCGAACC GTAGCGGATA GACGCATCAT CTTCAACCTG GCCGGGAACG AGGATC 356

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCGCTTT CAGTTTCCGT ACCGGTGGCA TCAGTCAAGT CCGTTTTGTG CACCAAACCG 60
CGTCCATATG AAACATAAAA CAAATCGCTT AAGCCCAAAG GGTTATCGAA CGATAAAGCG 120
ACATTTCTT GATATTTGCC GGTCGTTTTG CCGCCCGCAT CATCTATACC GATACTGAAC 180
CGTATGGGTT TATTCTGCTG CCATTGATC 210

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCCCGAAA CGCAATTGGT CGAAAGCTAT ATGCTGAACG ATGTGTTGCG GTTTTGGGAC 60

AGCGCAGGTT TGGGCGATGG GAAAGAAGCC GACCGCGCCC ATCGGCAAAA ACTGATTGAT 120

GTCCTGTCTA AAACCTATAC TCATTCGGAT GGGCAGTGGG GCTGGATAGA TTTGGTGTTC 180

GTTATCCTTG ACGGCAGCTC CCGCGATTTC GGTACGGCCT ATGATTTGTT GAGGGATGTT 240

ATCCTTAAAA TGATTGATC 259

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATCAAATGG ATGATTTATA TAGAATTTTC TTTTACGACT GCGTGCCGTT TGAAAAGAAA 60

ATGCACAATC CCGTATCTCA TCGTGCCATA GATTTTTCAA AGACTCCGGA AGCCATATTT 120

CGTTGCAATC TGCATACCGA ATTGAAGAAG AAGCGTAAAT TAGCGTTACG TTTAGGCAAG 180

CTGTCGGACA ATACAGCATG GATATTAAAA CCCCAAGTCA TGAAAAATCT TCTGAAAAAC 240

CCGTCAACTC AAATTACGGA AAACGATGTC GTGCTCGATG TTAAACAAAA AGGTGTAGAT 300

ATGCGTATAG GCTTGGATAT TTCATCTATT ACCTTAAAAA AACAAGCCGA TAAAATCATC 360

TTGTTTTCTG GTGATTCCGA TTTTGTCCCA GCAGCCAAAT TAGCCAGACG GGAAGGTATC 420

GATTTTATTC TTGATC 436

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATCGTTTTA CGTCGCAATC GAGCTTTGTG GTGCGCTCGC CTAAAGCCA ATCTTCTCTC 60

AATGGCCTGG GTGCCATTTT GCAGGGCACA GGTTTGGCCC GTGCGCAAGA CGATATTTAT 120

ACCGTGCAGG AATATATGCA GTCGCGTTCG GCTTTGGATG CGTTGCGTAA GAAAATGCCC 180

ATTCGCGATT TTTATGAAAA AGAAGGCGAT ATTTTCAGCC GTTTTAATGG TTTTGGCCTG 240

CGTGGCGAGG ATGAGGCGTT TTATCAATAC TACCGTGATA AGGTATCCAT CCATTTTGAC 300

TCTGTCTCAG GCATTTCCAA TTTGAGCGTT ACATCGTTTA ATGCCGGTGA ATCTCAAAAAG 360

ATC 363

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATCTTGCGT CATTATATC TTCACCGATA TTGCAATTAC CGCCGTTCCA GTTGAAATAA 60
 CAACGACTAA AATTGTAGTT CCTAAAAGAA TCATTCCTAT TCTTGCGTAC CATTTCCTAA 120
 TAATTGCGCC CGACAATTTT CATTTAATGC TCCATCAGTT CTTTACTTC CGGAAATCTG 180
 CTGTAATCTG ACATAAGACG CATAATTGAA CTATCAACGC CGTAACAGCC ATAGGTTTTA 240
 ATACCGTTTT CGGCGTGTTT CCAAATGCAA TTACTGTATT CGTAGCCTTT TACAAATTTA 300
 TCGGTTTCGG GATC 314

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCATACGA ATCTACCCTA AAATACCCCG TCGCCGATTT AGGATTGGCT ACATAAAGCT 60
 CATTATAAGG GTATTTTGAT GACATGATAC GGTTAAATTC ATTGCCGTTG TTTATCCTGA 120
 TTCTATAAAT TGGTTCAACA GCAAAGCCTC TGGATTCCCT TAATTGATTA TAATATTGCC 180
 TGTATGTTTG TACATCATGT CTTGTCCACG GCTCTCCAGG AGTCCTCAGA ATAGCAATCC 240
 CGTTAAATTT CGGATC 256

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCCACGCC TGTGCCTACC TTGGCTTTTT GTTCGCCAAA CAAGGCATTT AAGGTTGAGG 60
 ACTTGCCGAC ACCTGTCGCA CCGACAAGCA AGACATCCAA ATGACGGAAA CCGGCTGCTG 120
 TGACTTTTTG CCCGATTTC AAAATACGGT AACGATGCAT ATGCGCTCCT ACCAGCCAAA 180
 AAAAGAAGCA ACCGTGCTAA TCGCCCCTCC AATCGCTTTT GCAGCACCGC CGATC 235

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATCCAACGG GCATCGCTGT CCTACTCGG TGTGGTTTGA CCGCTGATTT GTCCTTCTTC 60
 GTCAACTTCT ATGGCCTGAC GCTGTTTGCT GCCGGCGGTC TGGATAATGG TGGCATCAAC 120
 GACGGCGGCG GATGCTTCT CTATTTTCTAG GCCTTTTCTG GTCAGTTGGC AGTTAATCAG 180
 TTTGAGTAAT TCGGACAGGG TGTCGTCTTG CGCCAGCCAG TTGCGGTAGC GGCATAAGGT 240
 ACTGTAATCG GGGATGATC 259

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GATCTGTGCC GTTGATTTTA TCTTTCAGAT GCAGCATCGA ATATCGGAAA GCCAAATCAG 60
 CAATTCTTTT TGCATCGTGT GGATTTTGAG ACGGGCCTAA TGACCGTACC CGCTTAATAA 120
 AAAATGCACC GTCAATCAAA ATGGCGGTTT TCATATTGCT TCCCCTATAT TTGTCAAAGA 180
 TATAAAAAAG CCCTTGGGAT C 201

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AATTCAAAGG AGGCATTTGT TGCAAGAAAA GTACAAAGTG ATTTGCAAAA AGCATTGAAT 60
 GCTAGCAACT ATAACAAGCA GCAATATGCA AGACGTGCGG CAACAGCGTT AGAGAATGCT 120
 TCAAAATCAA AAGTTATGGC AGCGAATTCT TTTTGATCTA TCTTGTGCGA ACGGGTCAAA 180
 TATTCTTCGT ACATTGAGTT AATCGTACCA ATCGCCCTAA CCACATTTTC ATCAGAAAAT 240
 ATGGAAATAA TAGCATCCCT ATACGCACCT AGTGTAATAT TGTTTCTATT ATTAGTTATA 300

GCATTATTCG AATACATAAT AGCACCTCCA AATT

334

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATTCCTGCG CACCTTTGCC GATGGGGAGA TAATCGCCTT TTTGCAGCAT TCTGCCCTGA 60

TGGCCGCCGA AACCGGCTTT CAGGTCGGTA CTTCTCGAAC CCATCACTTC CGGCACATCA 120

AATCCGCCCCG CCACGCACAC ATAGCCGTAC ATGCCCTGCA CGGCACGCAC CAGTTTCAAG 180

GTCTGCCCTT TGCGGGCGGT ATAACGCCAA TACGAATAGA CCGGTTTCGCC GTCCAATT 238

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AATTGGGCGA GATGCTGCCG GAAACGGATT TAAACAGAT TCGGGCGGCA GTGTTGAAGA 60
 CGAACGATGA GCGGCATTG CAGAAGGTGG TGAAAACGGC CAAAGGCAAT GCGCGGAAAC 120
 TGTCGAAGCT GCTGCTGATT GTGGACTATT TGTTCAGGT TAACCCTGAT GTTGATTTGG 180
 ATGATGATGT AATCGAACAC GCGGAAACCT ATTTAATCCA CTAAACCTTT GACAGATAAG 240
 GCAATAATT 249

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AATTTATGTA CGGTTTTGCC GTTTCAGTC AGCCAGTCGG CAAGGCGCAG AAAAAATCG 60
 CCGACAGGGC CTTGAAGCAG CAGGATATTT TCTGCGCTTT CAAGCAGGTT TTGCAGGTTA 120
 TTTTGTAGGA CGGTCTGTTT CATGTTGCAA TGTGGTTTTG TTTTATATGT AATAGTTTTA 180
 GGTGAACTT TCAAGCATAC GCCAAGAGAA TT 212

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AATTCAGTGC CTGCGTCATA TCACGGCTAC CTTGTGGTTC AGGGTTACTG TATCGCCCGC 60
 GGCATCGACG GCTTCAATAT GCAGCTTCAG CCAGCCGTGC TCGGGGGCGG ATGCGGTAC 120
 TTGGATGGAT TGGGCGCGTT TGGACTGAAT CACGGGCTGC AAGGCTTGCT CGGCGTACTG 180
 TTTGGCCAGT ACTTCGATGC GCTTTAAATG CTTTGGCGG CGCAATT 227

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GATCCAGGAC TCAAAAACCG ATTCCTAAT AGAGTGTCTA ATATCCCAAT CTTTTTTACC 60
 CCCTCTGCTG TAGAATTGAT AGAGAAAGTT TGTCTATCTT TTTCATATAC CCATGCCTTC 120
 TTTTATCAT TGTAGCTAAC ATAACCGCCA AACAATGCTT CTAGATC 167

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AATTCTTGCG GCCATTCCT GAATGGCTTT AGTCAAAACG GGGATGAACG TTTCGTATTC 60
 GACGGTGTAG GTATCGTTTG TTTTATTTAC CATCGGCAAT CGACCATATT CATCTTCCAG 120
 CGCAGCAATG TCCTGGGCAA TAAACCAATG CCGCAACCGA TCTTCTTTAT GACTGCCGTC 180
 CTTGATTGGA TTCGCCCACC ATTCGCGGAC TTTGTCCGCT CGTTCATCTG CCGGCAAGTC 240
 TTTGAATAAT T 251

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

| | |
|--|-----|
| AATTCCCGAC TATCGCGGAT GCGTAGTTTT TGCCGGTGGG CAAGAGCAGG TGTGGGATAA | 60 |
| GTTAGGTGAT TTGCCCCGATG GCGTCAGCCT GACCCCGCCT GAATCGGTAA ATATTGACGG | 120 |
| CTTAAAATCC GTAAAACTCG TCGCATTAAA TGCTGCCGCT CAGGCTTTTA TTAACAAGCA | 180 |
| CGCCGGTATC GACAGCGTAC CTGAATT | 207 |

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | |
|---|----|
| AATTGTTTGG GAATAATCCA AACAAACAGC ATCAGGATAG CGGCGGCGGT CAGGCTGCCT | 60 |
|---|----|

GAAAGGATTT TGCCGGGGTT TTTTGTAGGC AAAGCGGACG AGAAACCAAA GCAACAGCAG 120
 CATGGTGTCC CAATAGCCGA TTGAGAATAG GATGGCCAAA CCTTCTAGGA AATGGCGTAA 180
 ATCGTTTGTG GTAACCATGG GTAGTTCCTG TGGTTAAATG TGCAGGCTGC TTTTGCCGA 240
 ACCTTGCCGC ATCTCAAAAG CAGCCTGCGC TTCAGCGTTG CGTTACGCAG TAAAATAATG 300
 AATATTTGTA ACGGCTTGGG TATTTTTTGT CAATATTCCC GCCCTTCCCT TAACAGCTGC 360
 CGCGCTTTCC GTTAAAATT 379

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTCGCCGA AATCAGGCTG CTGCTCGATA ATCGGCGCGG CCGATTGGCG TTGTGCCTCG 60
 ATTAAATCCA TCTTGTCTTG CAGACGTTTG GCCTGGCCTT TGCGGCGGCG TTCGGCCAGT 120
 TGTTCCATCC GCGTTTCCGC AAATGCCGCC CGTTTGTGTC CGTTGAATAC CGCTTTGCAA 180
 ATCACCTTGC CCTGCATATC CTTACAATC ACATGGTCGG CATCGTGGAT GTCGTAAGCC 240
 ACCCGTACCT TCTGACCGCT GTAATCCAGC AATT 274

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AATTCCGTTC TTATTGGGCT TTTTCCATCC ATCGGGTATG CCTGAAGGGA ACGCAAACCC 60
 TGCCACTTGC CCATCGCTCC ATTCCCGCAT TAGCGCGTCT GACGGCAAGT GTTCTCGCGC 120
 CCAATCAAGC CACGCCTGCC GCATTGCGGC CTTGTCCTGC TGAAAACTTC GCAGTGCTTT 180
 TGCAACCGGC CCATCATTA CTTCAATCAA ATAAATCATT ATATTGCGT TCATTTTTC 240
 TACACCTTCG CCACATCCAA ATT 263

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AATTGTTCAA GAAAAAAGTC GGCACGGCGC GGCAACGGGG AAAATGCGTT GACGCCGTCT 60
 TTTTCTAAGG TGATGTAGTA GGGGCGGAAA TAGCCTTCTT CAAACGCCCA GAAACTGGCT 120
 TGGTTTTTCGT TTGCAATGCG TTTTGCAATG ACGTGATAAG GCGTGTGTC GCCAAAGCAG 180
 ACAACGGCCT GGATGTGATG TTGAGTGATG TATTCTTGCA AAAACTCAGG AAAGGCGTCG 240
 TAGTTGTCGT TAAAAACAAC GGTATGCGCT TGAGTGGGCG GATAAAAATA GTCGTCGCCT 300
 GCATTAAAGT TGAATT 316

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AATTCAATCA ACGGAAAACA CATCAGCATC AAAACAACG GTGGTAATGC CGACTTAAAA 60
 AACCTTAACG TCCATGCCAA AAGCGGGGCA TTGAACATTC ATTCCGACCG GGCATTGAGC 120
 ATAGAAAATA CCAAGCTGGA GTCTACCCAT AATACGCATC TTAATGCACA ACACGAGCGG 180

GTAACGCTCA ACCAAGTAGA TGCCTACGCA CACCGTCATC TAAGCATTAC CGGCAGCCAG 240
 ATTTGGCAAA ACGACAAACT GCCTTCTGCC AACAAGCTGG TGGCTAACGG TGTATTGGCA 300
 CTCAATGCGC GCTATTCCCA AATT 324

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AATTATGCAA AAAAACGCAA CGCCGAAAAA CTGGCACCGC GCGGATATTG TTGCTGCTTT 60
 GAAAAAGAAA GGCTGGTCAC TTCGAGCACT TTCAATAGAA GCGGGGTTGT CGCCGAATAC 120
 GCTTAGAAGC GCACTGGCCG CCCCTTATCT TAAGGGAGAA AGGATTATTG CCGCTGCAAT 180
 CGGAGTGGAA CCGGAAGAGA TTTGGTCCGA ACGGTATGCA GATCGGAATT 230

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

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AATTTAATCG GTGGAATGCC TGTTCACCG CACCAATCCC GCTGAATACG GTTGCTAATC      60
TAATATGTGA ATCAGGTTTA AGAAAAGTTT TAGATTTCCA ACCTTGTTGA CTGGGAAAGA      120
GCAAAGTTTT TTGTAATCGA GTATCGTGTG TCTGTGCCAT TGTCGAAATA GTCATACTTA      180
TATCGTTCTG TTTATCTTAT CAATATGAAA ACTACATCGT TGATTGCCCT GACAATGCCT      240
TGGTCAATT                                         249

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(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

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AATTCTTGTC CCGGAGTCCA ACGTATATTT ACCCTCCTGC GAGCTAAAAG ACTATTATTC      60
TCCACTGCCA CAGTAGCCGC ATTCACCGCC GTATTCACAT CCCCTTTAAC CAATGCCACT      120

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GCGCTGCCTG CGATAATCTG CGAGTAGGCT ATGACTTTTT GCGTTCTTG GGGTGACAGT 180
 TTGCCTACAT CGCGTCCGTC CAACAGGGTT TCTCCACCA TCTCGCCGAC TGCCGCGCCG 240
 ATTGCGCCGT CCCGACATTT GCCTTTATTT GCTACGCCG ATGCACAGCC TGCTACGGCA 300
 TGGGCTATCT TGTGGGCAAT GTAGTCTTCG CTGAGATTAA ATT 343

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AATTCTTCAA ACATCGTTTC GATAATCGGG TCGGTGTACA CACTGATGCG GTCGCCCCGCA 60
 CGGCTTTGAC CGGCTCGGAA AATATAGGCG GTGGCTTTGC CGTCGGCGAT GTCGACGCAC 120
 CAACGCCAGA TGGCGTCTTC GGTATTCAAA CAATCACCCG CACAGCTTTC ACCTGCGCGG 180
 AATT 184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TATGCTCAAT CTCATTTTCA AAATGCAAAA CTTTCTGAT TTTTCTACT TTTTGCTCAA 60
 TATTAGGAAG GTTTTAGGCA ATTGAAAATT TTTTGCGCA TTTTATGCG TCAAATTCG 120

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TTAACAGACT | ATTTTTGCAA | AGGTCTCCGT | CTGTAAAAGC | AAGGATAGGG | CATCTGCCCT | 180 |
| TTTGATTGTT | TGATTAACGA | TACAAGGAGT | TTCAAAATGA | GAGTTTTATA | GTGGATTAAC | 240 |
| AAAAACCAGT | ACAGCGTTGC | CTCGCCTTGC | CGTACTATTT | GTACTGTCTG | CGGCTTCGTC | 300 |
| GCCTTGTCCT | GATTTAAATT | TAATCCACTA | TATGTGTTCA | TGAAATGACT | TGGGTCGGAG | 360 |
| GCTCAGGTAA | TGCGCAACAA | AGTTCATATT | ATTGCGAAAT | TTGCGAATCT | GCAGGGCTTA | 420 |
| ACGATACGGG | AAATCCTGAT | AAATCTTTAG | GATTGCCAAA | CAATACGTTC | AGTAATCCGC | 480 |
| CTGGTTGGGG | AGCTACAATC | GGAGCTTTAG | CAGGTAGCCG | CATAGGTATG | CCTGAATTTG | 540 |
| GTACGTTTGC | GAGCCATGCC | ATTGAAAATT | TCGACTGGTC | ATGGTATCGA | CGTTATAGGG | 600 |
| AAATTGCCGA | AACGATTGAA | CGAGAATATT | CAGGCGGTTT | GCCTTAATAG | TTGAGGAGGT | 660 |
| CATGATGTTT | GCCAAACATT | ATCAATTCAT | CGCACTCGGC | ATCATGCTGC | TTCTTTATAT | 720 |
| GTTGATTCTC | TATACGACCG | ATTTTTCCAA | TCTGACGTAT | TGGATGCTGT | TTTTTATCTG | 780 |
| TTTTATTACA | GGAAAAATAT | TAGCTCGTTT | GTTAGAGAAA | AGCTTTAAAT | AAAATAGCAG | 840 |
| CTAGTCGCAA | AAGGTCGTCT | GAAACCTTTT | CAGGCGGCCT | TTCTAAAATA | CATCCAACTT | 900 |
| CCTAATCCCT | ATTTTTTCAA | AAGGAAATCT | ATGCCCCATC | TGCAAAACCT | GTCTTTGGGC | 960 |
| TTAAAGAAAA | AGCTGCCTGT | TATCCTGCAA | ACAGAAATAT | CAGAATGCGG | CTTGGCATGT | 1020 |
| CTGGCGGCTG | TGGCGGGATT | TCATGGTTTC | CATACGAATT | TACGCGCACT | GCGTTCAAAA | 1080 |
| TACTGTCCGA | GACCTTTGCA | AAATTCCCCA | AAATCCCCTA | AATGTCTTGG | TGGGAATTTT | 1140 |
| GGGGAATTTT | GCAAAGGTCT | CATTCTATAA | CTGTAAATAC | TTTTAAATTT | ATGACAAAAT | 1200 |
| AGTAAATATT | GCTAAAATAA | TATTGATGTC | ATGAAATTTT | TTCCTGCTCC | ATGTCTGTTG | 1260 |

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|--|------|
| GTTATCCTGG CTGTCATACC CCTTAAAACC TTAGCTGCCG ATGAAAACGA TGCAGAACTT | 1320 |
| ATCCGTTCCA TGCAGCGTCA GCAGCACATA GATGCTGAAT TGTAACTGA TGCAAATGTC | 1380 |
| CGTTTCGAGC AACCATTGGA GAAGAACAAT TATGTCCTGA GTGAAGATGA AACACCGTGT | 1440 |
| ACTCGGGTAA ATTACATTAG TTTAGATGAT AAGACGGCGC GCAAATTTTC TTTTCTTCCT | 1500 |
| TCTGTGCTCA TGAAAGAAAC AGCTTTTAAA ACTGGGATGT GTTTAGGTTC CAATAATTTG | 1560 |
| AGCAGGCTAC AAAAAGCCGC GCAACAGATA CTGATTGTGC GTGGCTACCT CACTTCCCAA | 1620 |
| GCTATTATCC AACCACAGAA TATGGATTCTG GGAATTCTGA AATTACGGGT ATCAGCAGGC | 1680 |
| GAAATAGGGG ATATCCGCTA TGAAGAAAA CGGGATGGGA AGTCTGCCGA GGGCAGTATT | 1740 |
| AGTGCATTCA ATAACAAATT TCCCTTATAT AGGAACAAAA TTCTCAATCT TCGCGATGTA | 1800 |
| GAGCAGGGCT TGGAAAACCT GCGTCGTTTG CCGAGTGTTA AAACAGATAT TCAGATTATA | 1860 |
| CCGTCCGAAG AAGAAGGCAA AAGCGATTTA CAGATCAAAT GGCAGCAGAA TAAACCCATA | 1920 |
| CGGTTTCAGTA TCGGTATAGA TGATGCGGGC GGCAAAACGA CCGGCAAATA TCAAGGAAAT | 1980 |
| GTCGCTTTAT CGTTCGATAA CCCTTTGGGC TTAAGCGATT TGTTTTATGT TTCATATGGA | 2040 |
| CGCGGTTTGG TGCACAAAAC GGAATTGACT GATGCCACCG GTACGGAAAAC TGAAAGCGGA | 2100 |
| TCCAGAAGTT ACAGCGTGCA TTATTCCGTG CCCGTAAAAA AATGGCTGTT TTCTTTTAAT | 2160 |
| CACAATGGAC ATCGTTACCA CGAAGCAACC GAAGGCTATT CCGTCAATTA CGATTACAAC | 2220 |
| GGCAAACAAT ATCAGAGCAG CCTGGCCGCC GAGCGCATGC TTTGGCGTAA CAGGTTTCAT | 2280 |
| AAAACCTCAG TCGGAATGAA ATTATGGACA CGCCAAACCT ATAAATACAT CGACGATGCC | 2340 |
| GAAATCGAAG TGCAACGCCG CCGCTCTGCA GGCTGGGAAG CCGAATTGCG CCACCGTGCT | 2400 |

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| TACCTCAACC GTTGGCAGCT TGACGGCAAG TTGTCTTACA AACGCGGGAC CGGCATGCGC | 2460 |
| CAAAGTATGC CCGCACCTGA AGAAAACGGC GGCGGTACTA TTCCAGGCAC ATCCCGTATG | 2520 |
| AAAATCATAA CCGCCGGATT GGATGCAGCG GCCCCGTTTA TGTTGGGCAA ACAGCAGTTT | 2580 |
| TTCTACGCAA CCGCCATTCA AGCTCAATGG AACAAAACGC CTTTGGTTGC CCAAGACAAG | 2640 |
| TTGTCTATCG GCAGCCGCTA CACCGTTCGC GGATTTGATG GGGAGCAGAG TCTTTTCGGA | 2700 |
| GAGCGAGGTT TCTACTGGCA GAATACTTTA ACTTGGTATT TTCATCCGAA CCATCAGTTC | 2760 |
| TATCTCGGTG CGGACTATGG CCGCGTATCT GGCGAAAGTG CACAATATGT ATCGGGCAAG | 2820 |
| CAGCTGATGG GTGCAGTGGT CGGCTTCAGA GGAGGGCATA AAGTAGGCGG TATGTTTGCT | 2880 |
| TATGATCTGT TTGCCGGCAA GCCGCTTCAT AAACCCAAAG GCTTTCAGAC GACCAACACC | 2940 |
| GTTTACGGCT TCAACTTGAA TTACAGTTTC TAACCTCTGA ATTTTTTTTAC TGATATTTAG | 3000 |
| ACGGTCTTTC CTTATCCTCA GACTGTCAAA CTTTACCTAC GTACTTGGCG CGCAGTACGT | 3060 |
| TCATCTTCAA AATGGAATAG ACATGAATAA AGGTTTACAT CGCATTATCT TTAGTAAAAA | 3120 |
| GCACAGCACC ATGGTTGCAG TAGCCGAAAC TGCCAACAGC CAGGGCAAAG GTAAACAGGC | 3180 |
| AGGCAGTTCG GTTTCTGTTT CACTGAAAAC TTCAGGCGAC CTTTGCGGCA AACTCAAAAC | 3240 |
| CACCCTTAAA ACCTTGGTCT GCTCTTTGGT TTCCCTGAGT ATGGTATTGC CTGCCCATGC | 3300 |
| CCAAATTACC ACCGACAAAT CAGCACCTAA AAACCAGCAG GTCGTTATCC TTAAACCAA | 3360 |
| CACTGGTGCC CCCTTGGTGA ATATCCAAAC TCCGAATGGA CGCGGATTGA GCCACAACCG | 3420 |
| CTATACGCAG TTTGATGTTG ACAACAAAGG GGCAGTGTTA AACACGACC GTAACAATAA | 3480 |
| TCCGTTTCTG GTCAAAGGCA GTGCGCAATT GATTTTGAAC GAGGTACGCG GTACGGCTAG | 3540 |

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|-------------|------------|------------|------------|-------------|------------|------|
| CAAACCTCAAC | GGCATCGTTA | CCGTAGGCGG | TCAAAAGGCC | GACGTGATTA | TTGCCAACCC | 3600 |
| CAACGGCATT | ACCGTTAATG | GCGGCGGCTT | TAAAAATGTC | GGTCGGGGCA | TCTTAACTAT | 3660 |
| CGGTGCGCCC | CAAATCGGCA | AAGACGGTGC | ACTGACAGGA | TTTGATGTGC | GTCAAGGCAC | 3720 |
| ATTGACCGTA | GGAGCAGCAG | GTTGGAATGA | TAAAGGCGGA | GCCGACTACA | CCGGGGTACT | 3780 |
| TGCTCGTGCA | GTTGCTTTGC | AGGGGAAATT | ACAGGGTAAA | AACCTGGCGG | TTTCTACCGG | 3840 |
| TCCTCAGAAA | GTAGATTACG | CCAGCGGCGA | AATCAGTGCA | GGTACGGCAG | CGGGTACGAA | 3900 |
| ACCGACTATT | GCCCTTGATA | CTGCCGCACT | GGGCGGTATG | TACGCCGACA | GCATCACACT | 3960 |
| GATTGCCAAT | GAAAAAGGCG | TAGGCGTCAA | AAATGCCGGC | ACACTCGAAG | CGGCCAAGCA | 4020 |
| ATTGATTGTG | ACTTCGTCAG | GCCGCATTGA | AAACAGCGGC | CGCATCGCCA | CCACTGCCGA | 4080 |
| CGGCACCGAA | GCTTCACCGA | CTTATCTCTC | CATCGAAACC | ACCGAAAAAG | GAGCGGCAGG | 4140 |
| CACATTTATC | TCCAATGGTG | GTCGGATCGA | GAGCAAAGGC | TTATTGGTTA | TTGAGACGGG | 4200 |
| AGAAGATATC | AGCTTGCGTA | ACGGAGCCGT | GGTGCAGAAT | AACGGCAGTC | GCCCAGCTAC | 4260 |
| CACGGTATTA | AATGCTGGTC | ATAATTTGGT | GATTGAGAGT | AAAACATAATG | TGAACAATGC | 4320 |
| CAAAGGCTCG | GCTAATCTGT | CGGCCGGCGG | TCGTACTACG | ATCAATGATG | CTACTATTCA | 4380 |
| AGCGGGCAGT | TCCGTGTACA | GCTCCACCAA | AGGCGATACT | GAATTGGGTG | AAAATACCCG | 4440 |
| TATTATTGCT | GAAAACGTAA | CCGTATTATC | TAACGGTAGT | ATTGGCAGTG | CTGCTGTAAT | 4500 |
| TGAGGCTAAA | GAACTGCAC | ACATTGAATC | GGGCAAACCG | CTTCTTTAG | AAACCTCGAC | 4560 |
| CGTTGCCTCC | AACATCCGTT | TGAACAACGG | TAACATTAAA | GGCGGAAAGC | AGCTTGCTTT | 4620 |
| ACTGGCAGAC | GATAACATTA | CTGCCAAAAC | TACCAATCTG | AATACTCCCG | GCAATCTGTA | 4680 |

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|------------|------------|------------|------------|------------|------------|------|
| TGTTCATACA | GGTAAAGATC | TGAATTTGAA | TGTTGATAAA | GATTTGTCTG | CCGCCAGCAT | 4740 |
| CCATTTGAAA | TCGGATAACG | CTGCCCATAT | TACCGGCACC | AGTAAAACCC | TCACTGCCTC | 4800 |
| AAAAGACATG | GGTGTGGAGG | CAGGCTTGCT | GAATGTTACC | AATACCAATC | TGCGTACCAA | 4860 |
| CTCGGGTAAT | CTGCACATTC | AGGCAGCCAA | AGGCAATATT | CAGCTTCGCA | ATACCAAGCT | 4920 |
| GAACGCAGCC | AAGGCTCTCG | AAACCACCGC | ATTGCAGGGC | AATATCGTTT | CAGACGGCCT | 4980 |
| TCATGCTGTT | TCTGCAGACG | GTCATGTATC | CTTATTGGCC | AACGGTAATG | CCGACTTTAC | 5040 |
| CGGTCACAAT | ACCCTGACAG | CCAAGGCCGA | TGTCAATGCA | GGATCGGTTG | GTAAAGGCCG | 5100 |
| TCTGAAAGCA | GACAATACCA | ATATCACTTC | ATCTTCAGGA | GATATTACGT | TGGTTGCCGG | 5160 |
| CAACGGTATT | CAGCTTGGTG | ACGGAAAACA | ACGCAATTCA | ATCAACGGAA | AACACATCAG | 5220 |
| CATCAAAAAC | AACGGTGGTA | ATGCCGACTT | AAAAAACCTT | AACGTCCATG | CCAAAAGCGG | 5280 |
| GGCATTGAAC | ATTCATTCCG | ACCGGGCATT | GAGCATAGAA | AATACCAAGC | TGGAGTCTAC | 5340 |
| CCATAATACG | CATCTTAATG | CACAACACGA | GCGGGTAACG | CTCAACCAAG | TAGATGCCTA | 5400 |
| CGCACACCGT | CATCTAAGCA | TTACCGGCAG | CCAGATTTGG | CAAAACGACA | AACTGCCTTC | 5460 |
| TGCCAACAAG | CTGGTGGCTA | ACGGTGTATT | GGCACTCAAT | GCGCGCTATT | CCCAAATTGC | 5520 |
| CGACAACACC | ACGCTGAGAG | CGGGTGCAAT | CAACCTTACT | GCCGGTACCG | CCCTAGTCAA | 5580 |
| GCGCGGCAAC | ATCAATTGGA | GTACCGTTTC | GACCAAGACT | TTGGAAGATA | ATGCCGAATT | 5640 |
| AAAACCATTG | GCCGGACGGC | TGAATATTGA | AGCAGGTAGC | GGCACATTAA | CCATCGAACC | 5700 |
| TGCCAACCGC | ATCAGTGCGC | ATACCGACCT | GAGCATCAAA | ACAGGCGGAA | AATTGCTGTT | 5760 |
| GTCTGCAAAA | GGAGGAAATG | CAGGTGCGCC | TAGTGCTCAA | GTTTCCTCAT | TGGAAGCAAA | 5820 |

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|------------|------------|------------|------------|-------------|-------------|------|
| AGGCAATATC | CGTCTGGTTA | CAGGAGAAAC | AGATTTAAGA | GGTTCTAAAA | TTACAGCCGG | 5880 |
| TAAAAACTTG | GTTGTCGCCA | CCACCAAAGG | CAAGTTGAAT | ATCGAAGCCG | TAAACAACCTC | 5940 |
| ATTGAGCAAT | TATTTTCCTA | CACAAAAAGC | GGCTGAACTC | AACCAAAAAAT | CCAAAGAATT | 6000 |
| GGAACAGCAG | ATTGCGCAGT | TGAAAAAAG | CTCGCCTAAA | AGCAAGCTGA | TTCCAACCCT | 6060 |
| GCAAGAAGAA | CGCGACCGTC | TCGCTTTCTA | TATTCAAGCC | ATCAACAAGG | AAGTTAAAGG | 6120 |
| TAAAAAACC | AAAGGCAAAG | AATACCTGCA | AGCCAAGCTT | TCTGCACAAA | ATATTGACTT | 6180 |
| GATTTCCGCA | CAAGGCATCG | AAATCAGCGG | TTCCGATATT | ACCGCTTCCA | AAAAACTGAA | 6240 |
| CCTTCACGCC | GCAGGCGTAT | TGCCAAAGGC | AGCAGATTCA | GAGGCGGCTG | CTATTCTGAT | 6300 |
| TGACGGCATA | ACCGACCAAT | ATGAAATTGG | CAAGCCCACC | TACAAGAGTC | ACTACGACAA | 6360 |
| AGCTGCTCTG | AACAAGCCTT | CACGTTTGAC | CGGACGTACG | GGGGTAAGTA | TTCATGCAGC | 6420 |
| TGCGGCACTC | GATGATGCAC | GTATTATTAT | CGGTGCATCC | GAAATCAAAG | CTCCCTCAGG | 6480 |
| CAGCATAGAC | ATCAAAGCCC | ATAGTGATAT | TGTACTGGAG | GCTGGACAAA | ACGATGCCTA | 6540 |
| TACCTTCTTA | AAAACCAAAG | GTAAAAGCGG | CAAAATCATC | AGAAAAACCA | AGTTTACCAG | 6600 |
| CACCCGCGAC | CACCTGATTA | TGCCAGCCCC | CGTCGAGCTG | ACCGCCAACG | GTATCACGCT | 6660 |
| TCAGGCAGGC | GGCAACATCG | AAGCTAATAC | CACCCGCTTC | AATGCCCCCTG | CAGGTAAAGT | 6720 |
| TACCCTGGTT | GCGGGTGAAG | AGCTGCAACT | GCTGGCAGAA | GAAGGCATCC | ACAAGCACGA | 6780 |
| GTTGGATGTC | CAAAAAAGCC | GCCGCTTTAT | CGGCATCAAG | GTAGGTAAGA | GCAATTACAG | 6840 |
| TAAAAACGAA | CTGAACGAAA | CCAAATTGCC | TGTCCGCGTC | GTCGCCCAAA | CTGCAGCCAC | 6900 |
| CCGTTCAGGC | TGGGATACCG | TGCTCGAAGG | TACCGAATTC | AAAACCACGC | TGGCCGGTGC | 6960 |

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|------------|------------|------------|------------|------------|------------|------|
| CGACATTCAG | GCAGGTGTAG | GCGAAAAAGC | CCGTGTCGAT | GCGAAAATTA | TCCTCAAAGG | 7020 |
| CATTGTGAAC | CGTATCCAGT | CGGAAGAAAA | ATTAGAAACC | AACTCAACCG | TATGGCAGAA | 7080 |
| ACAGGCCGGA | CGCGGCAGCA | CTATCGAAAC | GCTAAAACTG | CCCAGCTTCG | AAAGCCCTAC | 7140 |
| TCCGCCCAAA | TTGTCCGCAC | CCGGCGGCTA | TATCGTCGAC | ATTCCGAAAG | GCAATCTGAA | 7200 |
| AACCGAAATC | GAAAAGCTGT | CCAAACAGCC | CGAGTATGCC | TATCTGAAAC | AGCTCCAAGT | 7260 |
| AGCGAAAAAC | ATCAACTGGA | ATCAGGTGCA | GCTTGCTTAC | GACAGATGGG | ACTACAAACA | 7320 |
| GGAGGGCTTA | ACCGAAGCAG | GTGCGGCGAT | TATCGCACTG | GCCGTTACCG | TGGTCACCTC | 7380 |
| AGGCGCAGGA | ACCGGAGCCG | TATTGGGATT | AAACGGTGCG | GCCGCCGCCG | CAACCGATGC | 7440 |
| AGCATTCGCC | TCTTTGGCCA | GCCAGGCTTC | CGTATCGTTC | ATCAACAACA | AAGGCGATGT | 7500 |
| CGGCAAAACC | CTGAAAGAGC | TGGGCAGAAG | CAGCACGGTG | AAAAATCTGG | TGGTTGCCGC | 7560 |
| CGCTACCGCA | GGCGTAGCCG | ACAAAATCGG | CGCTTCGGCA | CTGAACAATG | TCAGCGATAA | 7620 |
| GCAGTGGATC | AACAACCTGA | CCGTCAACCT | AGCCAATGCG | GGCAGTGCCG | CACTGATTAA | 7680 |
| TACCGCTGTC | AACGGCGGCA | GCCTGAAAGA | CAATCTGGAA | GCGAATATCC | TTGCGGCTTT | 7740 |
| GGTCAATACC | GCGCATGGAG | AAGCAGCCAG | TAAAATCAAA | CAGTTGGATC | AGCACTACAT | 7800 |
| AGTCCACAAG | ATTGCCCATG | CCATAGCGGG | CTGTGCGGCA | GCGGCGGCGA | ATAAGGGCAA | 7860 |
| GTGTCAGGAT | GGTGCGATAG | GTGCGGCTGT | GGGCGAGATA | GTCGGGGAGG | CTTTGACAAA | 7920 |
| CGGCAAAAAT | CCTGACACTT | TGACAGCTAA | AGAACGCGAA | CAGATTTTGG | CATACAGCAA | 7980 |
| ACTGGTTGCC | GGTACGGTAA | GCGGTGTGGT | CGGCGGCGAT | GTAAATGCGG | CGGCGAATGC | 8040 |
| GGCTGAGGTA | GCGGTGAAAA | ATAATCAGCT | TAGCGACAAA | GAGGGTAGAG | AATTTGATAA | 8100 |

| | |
|---|------|
| CGAAATGACT GCATGCGCCA AACAGAATAA TCCTCAACTG TGCAGAAAAA ATACTGTAAA | 8160 |
| AAAGTATCAA AATGTTGCTG ATAAAAGACT TGCTGCTTCG ATTGCAATAT GTACGGATAT | 8220 |
| ATCCCGTAGT ACTGAATGTA GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT | 8280 |
| TCATTCATCT TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTCAG | 8340 |
| CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTTGAATA CTGCTGCTAA | 8400 |
| ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA TGGATGTCCG ACCAAGGTTA | 8460 |
| TACACTTATT TCAGGAGTTA ATCCTAGATT CATTCCAATA CCAAGAGGGT TTGTAAAACA | 8520 |
| AAATACACCT ATTACTAATG TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTAAA | 8580 |
| AAGACATCTG GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCCATAA | 8640 |
| CCGCACCAAT TTTATGGCAG AACTAAATTC ACGAGGAGGA CGCGTAAAAT CTGAAACCCA | 8700 |
| AACTGATATT GAAGGCATTA CCCGAATTAA ATATGAGATT CCTACACTAG ACAGGACAGG | 8760 |
| TAAACCTGAT GGTGGATTTA AGGAAATTTC AAGTATAAAA ACTGTTTATA ATCCTAAAAA | 8820 |
| ATTTTCTGAT GATAAAATAC TTCAAATGGC TCAAATGCT GCTTCACAAG GATATTCAAA | 8880 |
| AGCCTCTAAA ATTGCTCAAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT | 8940 |
| TCAATTCTCA GAAACCTTTG ACGGAATCAA ATTTAGATCA TATTTTGATG TAAATACAGG | 9000 |
| AAGAATTACA AACATTCACC CAGAATAATT TAAAGGAAAA ATTATGAAAA ATAATATTTT | 9060 |
| TCTAACTTA AATAAAAAAT CTATAAATAA CAACCATTTT GTTATTTTGA TTTTTTTTGA | 9120 |
| AACAATTTAC CAATTTGAAA CTAAAGATAC GCTTTTAGAG TGTTTTAAAA ATATTACAAC | 9180 |
| TACCGGACAT TTTGGAGTAA TAGGTGCTCA ATATGAAAAA ATAGATGCTA CCAGATGGAT | 9240 |

TGGAGATTAT GAAGAGGTAA ATGGATTGTA GTATATTGAT AAAGCTCCTT CTATTTATTT 9300
 TTCAGTTGGA GATGATTTC A TCCTGAAGA ATTAATTATA CCTATTAATT TAGCATATCA 9360
 TTACTTTAAT ATTGCAATAT CTGATTTCTT AATAGCTCAC CCTGAATATC AAAAAAAGTG 9420
 TAAAGAAATA CAAAAAACAT ATTCTCAAAC AAAGTGTAGC CTGCATGAAA CCTAAAATCC 9480
 ATGCGTAAGG TGTGTGCTTC AGCACGCACG CGTTCCATGA TTTACGGCTC AATGCCGTCT 9540
 GAAAAGCTCA CAATTTTTC A GACGGCATT GTTATGCAAG TAAATATTCA GATTCCCTAT 9600
 ATACTGCCCA GACGCGTGCG TGCTGAAGAC ACCCCCTACG CTTGCTGCAG AACTTTCGGG 9660
 TAAACCGGT GTGAGCATT A GCGCACCGTA TGCCAATGAG AACAGTCGCA TCCTGCTCAG 9720
 CACCACGGAT ATCAGTTCGG AAAACGGCAA AATCAAAATT CAATCTTACG GTGACCAATA 9780
 TTACTATGCG AGACAGAGCG AACTCTATAC CTTTGAACGC CGCAGCTACA AACTGGCAA 9840
 ATGGTACAAC CGCAAACACA TTACCGAAGT CAAAGAACAC AAAACGCCA AGCCCGACGC 9900
 AGTAAACCTC AGCGCATCCC AAGGCATCGA CATCAAATCT GGTGGCAGCA TCGACGCCTA 9960
 CGCCACCGCA TTCGATGCCC CCAAAGGCAG CATTAAACATC GAAGCCGGGC GGAAATTGAC 10020
 ACTCTATGCC GTAGAAGAGC TCAACTACGA CAACTAGAC AGCCAAAAAA GGCGCAGATT 10080
 TCTCGGCATC AGCTACAGCA AAGCACACGA CACCACCACC CAAGTCATGA AAACCGCGCT 10140
 GCCCTCAAGG GTAGTTGCAG AATCAGCCAA CCTCCAATCG GGCTGGGATA CCAAAGTGA 10200
 AGGCACACAG TTTGAAACCA CACTGGGTGG CGCAACCATA CGCGCAGGCG TAGGTGAGCA 10260
 GGCACGGGCA GATGCCAAGA TTATCCTCGA AGGGATCAAA AGCAGCATCC ACACAGAAAC 10320
 CGTGAGCAGC AGCAAATCTA CTCTATGGCA AAAACAGGCA GGACGGGGCA GTAACATCGA 10380

AACCTTGCAA TTGCCGAGTT TCACCGGTCC CGTTGCGCCC GTACTGTCCG CACCCGGCGG 10440
TTACATTGTC GACATTCCGA AAGGCAATCT GAAAACCCAA ATCGAAACCC TCACCAAGCA 10500
GCCCCGAGTAT GCTTATTTGA AACAACTTCA AGTTGCGAAA AACATCAACT GGAATCAGGT 10560
GCAGCTTGCT TACGATAAAT GGGACTACAA ACAGGAGGGC ATGACACCCG CAGCAGCAGC 10620
TGTCGTCGTT ATCGTCGTAA CCGTATTGAC CTACGGTGCA CTGTCCGCCC CGGCAGCCGC 10680
CGGAACGGCG GCGCGGGCAG GCGCAGGAGC GGGAGGAGCC GCAGCAGGAA CGGCAGCCGG 10740
AACTGGAGTA GCAGCAGGAA CGGCAGCCAC AACC GGAGTA GCAGCAGGCA CATCAGCTGC 10800
AGCTATCACC ACAGCCGCAG GCAAAGCCGC ACTGGCCAGT CTCGCCAGCC AAGCCGCAGT 10860
TTCCCTCATC AACAAACAAAG GAGACATAAA CCATACCCTG AAAGAACTGG GCAAAGCAG 10920
CACCGTCAGA CAGGCCGCCA CCGCCGCCGT AACC GCAGGC GTACTGCAGG GCATAAGCGG 10980
GCTGAACACC CAAGCAGCCG AAGCCGTCAG CAAACATTTT CACAGTCCCG CAGCAGGCAA 11040
ACTGACCGCT AACCTGATCA ACAGCACCGC TGCCGCAAGT GTCCATACCG CCATCAACGG 11100
CGGCAGCCTG AAAGACAACT TGGGCGATGC CGCACTGGGT GCGATAGTCA GTACCGTACA 11160
CGGAGAAGTA GCGAGCAAAA TCAAATTTAA TCTCAGCGAA GACTACATTG CCCACAAGAT 11220
AGCCCATGCC GTAGCAGGCT GTGCATCGGC GGTAGCAAAT AAAGGCAAAT GTCGGGACGG 11280
CGCAATCGGC GCGGCAGTCG GCGAGATGGT GGGAGAAACC CTGTTGGACG GACGCGATGT 11340
AGGCAAACCTG TCACCCCAAG AACGCCAAAA AGTCATAGCC TACTCGCAGA TTATCGCAGG 11400
CAGCGCAGTG GCATTGGTTA AAGGGGATGT GAATACGGCG GTGAATGCGG CTACTGTGGC 11460
AGTGGAGAAT AATAGTCTTT TAGCTCGCAG GAGGGTAAAT ATACGTTGGA CTCCGCGACA 11520

AGAATTGGAA CATGAATATG CCATTCTTGA AATCCAGGCC ATTACCAATC AAATCCGAAG 11580
 GCTGGATCCG AAATTTAACG GGATTGCTAT TCTGAGGACT CCTGGAGAGC CGTGGACAAG 11640
 ACATGATGTA CAAACATACA GGCAATATTA TAATCAATTA AGGGAATCCA GAGGCTTTGC 11700
 TGTTGAACCA ATTTATAGAA TCAGGATAAA CAACGGCAAT GAATTTAACC GTATCATGTC 11760
 ATCAAAATAC CCTTATAATG AGCTTTATGT AGCCAATCCT AAATCGGCGA CGGGGTATTT 11820
 TAGGGTAGAT TCGTATGATC CTGCGACAAG GGAAATTATT TCAAGAAAAT TTACCCAATT 11880
 TTCTCAAATC CAAGAAAGTA CGGGGATTGG TTATATCAAG GAGGCTGTTA GAAAATATAG 11940
 CCCTGGTACT GTCATTTCCA ATGTTCCAAG TACACCTACT ACGATAAGAG GAAGAAAGCT 12000
 TGAAGGAAAA CTTATTTTAG AAGTTCCTGC TCAGGTCAAT CCAATTCCAC AATCTGTATT 12060
 AAGGGCGGCA CAAGAAGAAA ATGTTATCAT TAGAGATACA ACAGGAAGGA TTTACAAATG 12120
 AAGAAAGATA TTTTTTATTG TGAGCAGTGG TCTTATGGTT ATAAGAGACT TCATAAGCCT 12180
 TTTTCTGAGA AACAAGCTGA GGAAAAACAT CTTAAAGGGG AGTTATATAC TGCCGTAATA 12240
 GGTTCGGCGA CACAACCTGA ATATGTAATT ACCTTGCGAG AGGAAGTAGG TTTTTTTTCG 12300
 GTAAATTTTT TCGATAAATT TGGAAGGGAT TATTTAACCC ATCAATTTC AATATATTC 12360
 AATTCGAATT ATTATTTTCT TTCTATGGCT GTATGGAGAG ATTATATAAC TTTGGAATCT 12420
 CATGACTTAG CAGAAGGATA TACTTATTTT TCAATGAAA ATACGGATGA TTGCTATGTT 12480
 TTGAAACAAG ATTTTATTAA TAATGAGCGA TATGAAAAA CAGAATTATA TTCCCAAAAA 12540
 GATAAGGTAA TTCTATTTCC AAAGTTTGGT GAATATGATT TGGTGTTAAA TCCGGACATT 12600
 ATTTAATTAA GTTTTAAGGC CGTCTGAAAA AAATTTCAAA CGGCTTTTAT TATTGGGTTT 12660

REPLACEMENT SHEET (RULE 26)

ACTGACAAAC AATTGCTGAA AGCTATTGGC GAAGGAAGGG ACACGACAGG TAAAATGACC 13860
 GAGCAGTTAT TTGACTCTTT AGCTAAACAA AATGGCTTCA GAGTGCTTTC GGGCGGCAAA 13920
 TACGGCGGAA ATAACGGTTT TGATCATGTA TGGCAGGCTG CCGATGGTAG TGTCGTTTTG 13980
 ATTGTAGAAA GTAAGCAGAT TAGGAACGGT ACGGTACAGC TGAATCCGAA TGGTGCGGGT 14040
 GGATATACGC AAATGAGTGA GGATTGGATT AGACAAGTTT TAGATCAATT ACCCGATGGT 14100
 AGTCCCGCTA AAGCTGCTGT CTTCAAAGCA AATAAGAACG GCACATTAAA AACAGCAATA 14160
 GCAGGCGTTG ATCGTCAAAC AGGTAAGGCC GTTATTCTTC CTGTCAAAGT TCCTTCTAAA 14220
 ACCAATATAA GGAGATAACA ATGGGGCACA ATATGATGAC CACCCAAAAA TGGTATGAGC 14280
 ATATTACTAA TGTAATCATA GGCAATACTG CTAATTTCAA TAGCGGTTGC CTTGACTCTA 14340
 TAGATTATGT AGATGAAAGA AAAGGCGTTC CGCTTGCAGC TATGCAACAT ATTTTCATGG 14400
 ACGTTAGAGC TGCAGCTTCC CATGCCTATC TATTTGAACA TGATCTTAAG AAATTCAAGC 14460
 AATATGCTTA TGTTGCAGGA AAGCTGGGGG TTTTGCTGAG TGTAATTCT ACAGACCCTG 14520
 AACCCCTTCTT CTTTCCCTGT GACATGCTCA ACATTCAAAA TCCGATGTTT CTGATGCTGA 14580
 TGAGCGACAG CCCACAGCTG CGTGAGTTTC TGGTGCGCAA TATCGACAAC ATCGCCAACG 14640
 ATACAGAAGC CTTTATAAAC CGCTACGACC TCAACCGGCA TATGATTTAC AATACTCTGC 14700
 TGATGGTGGA GGGTAAGCAG CTTGATCGGT TGAAACAACG TAGCGAGAAA GTCTTGCGCGC 14760
 ATCCCACCCC TAGCAAATGG CTGCAAAGC GGTTGTACGA TTACCGCTTC TTCCTCGCTT 14820
 TCGCCGAACA GGATGCCGAG GCAATGAAAG CCGCCTTAGA GCCGCTTTTC GATAAAAAAA 14880
 CCGCGCGTAT GGCTGCCAAA GAAACATTGT CCTATTTCTGA TTTCTACCTG CAGCCGCAAA 14940

TCGTTACCTA CGCCAAAATC GCATCCATGC ACGGTTTCGA TTTGGGCATA GATCAAGAAA 15000

TCTCACCGAG GGATTTGATT GTTTACGATC CGCTGCCGGC AGACGAATAT CAAGACATCT 15060

TCGATTTTAT GAAACAGTAT GACTTGTCTT ACCCGTATGA ATATCTGCAG GATTGGATAG 15120

ATTACTATAC GTTCAAAACC GATAAGCTGG TATTTGGTAA CGCGAAGCGA GAGTGAGCCG 15180

TAAAACTCTG AGCTCCTGTT TTATAGATTA CAACTTTAGG CCGTCTTAAA GCTGAAAGAT 15240

TTTCGAAAGC TATAAATTGA AGCCCTTCCA CAGTACATAG ATCTGTGTTG TGGCGGGGCT 15300

TTACCACGCT GATTGCCGGA GAAGAACTCA ACCTGCTGGC AAAACAAGGC ATGAGATCTT 15360

TGCAATAACA TGAGTTGAGA CCTTTGCAAA AAAGCCCTTC CCCGACATCC GAAACCCAAA 15420

CACAGGATTT CGGCTGTTTT CGTACCAAAT ACCTCCTAAT TTTACCCAAA TACCCCTTA 15480

ATCCTCCTCG GACACCCGAT AATCAGGCAT CCGGGCTGCC TTTTAGGCGG CAGCGGGCGC 15540

ATTTAGCCTG TTGGCCGCTT TCAACAGGTT CAAACACATC GCCTTCAGGT GGCTTTGCGC 15600

ACTCACTTTG TCATTTCCAA 15620

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Phe | Pro | Ala | Pro | Cys | Leu | Leu | Val | Ile | Leu | Ala | Val | Ile | 1 | 5 | 10 | 15 |
| Pro | Leu | Lys | Thr | Leu | Ala | Ala | Asp | Glu | Asn | Asp | Ala | Glu | Leu | Ile | Arg | 20 | 25 | 30 | |
| Ser | Met | Gln | Arg | Gln | Gln | His | Ile | Asp | Ala | Glu | Leu | Leu | Thr | Asp | Ala | 35 | 40 | 45 | |
| Asn | Val | Arg | Phe | Glu | Gln | Pro | Leu | Glu | Lys | Asn | Asn | Tyr | Val | Leu | Ser | 50 | 55 | 60 | |
| Glu | Asp | Glu | Thr | Pro | Cys | Thr | Arg | Val | Asn | Tyr | Ile | Ser | Leu | Asp | Asp | 65 | 70 | 75 | 80 |
| Lys | Thr | Ala | Arg | Lys | Phe | Ser | Phe | Leu | Pro | Ser | Val | Leu | Met | Lys | Glu | 85 | 90 | 95 | |
| Thr | Ala | Phe | Lys | Thr | Gly | Met | Cys | Leu | Gly | Ser | Asn | Asn | Leu | Ser | Arg | 100 | 105 | 110 | |
| Leu | Gln | Lys | Ala | Ala | Gln | Gln | Ile | Leu | Ile | Val | Arg | Gly | Tyr | Leu | Thr | 115 | 120 | 125 | |
| Ser | Gln | Ala | Ile | Ile | Gln | Pro | Gln | Asn | Met | Asp | Ser | Gly | Ile | Leu | Lys | 130 | 135 | 140 | |
| Leu | Arg | Val | Ser | Ala | Gly | Glu | Ile | Gly | Asp | Ile | Arg | Tyr | Glu | Glu | Lys | 145 | 150 | 155 | 160 |
| Arg | Asp | Gly | Lys | Ser | Ala | Glu | Gly | Ser | Ile | Ser | Ala | Phe | Asn | Asn | Lys | 165 | 170 | 175 | |
| Phe | Pro | Leu | Tyr | Arg | Asn | Lys | Ile | Leu | Asn | Leu | Arg | Asp | Val | Glu | Gln | 180 | 185 | 190 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Glu | Asn | Leu | Arg | Arg | Leu | Pro | Ser | Val | Lys | Thr | Asp | Ile | Gln | 195 | 200 | 205 | |
| Ile | Ile | Pro | Ser | Glu | Glu | Glu | Gly | Lys | Ser | Asp | Leu | Gln | Ile | Lys | Trp | 210 | 215 | 220 | |
| Gln | Gln | Asn | Lys | Pro | Ile | Arg | Phe | Ser | Ile | Gly | Ile | Asp | Asp | Ala | Gly | 225 | 230 | 235 | 240 |
| Gly | Lys | Thr | Thr | Gly | Lys | Tyr | Gln | Gly | Asn | Val | Ala | Leu | Ser | Phe | Asp | 245 | 250 | 255 | |
| Asn | Pro | Leu | Gly | Leu | Ser | Asp | Leu | Phe | Tyr | Val | Ser | Tyr | Gly | Arg | Gly | 260 | 265 | 270 | |
| Leu | Val | His | Lys | Thr | Asp | Leu | Thr | Asp | Ala | Thr | Gly | Thr | Glu | Thr | Glu | 275 | 280 | 285 | |
| Ser | Gly | Ser | Arg | Ser | Tyr | Ser | Val | His | Tyr | Ser | Val | Pro | Val | Lys | Lys | 290 | 295 | 300 | |
| Trp | Leu | Phe | Ser | Phe | Asn | His | Asn | Gly | His | Arg | Tyr | His | Glu | Ala | Thr | 305 | 310 | 315 | 320 |
| Glu | Gly | Tyr | Ser | Val | Asn | Tyr | Asp | Tyr | Asn | Gly | Lys | Gln | Tyr | Gln | Ser | 325 | 330 | 335 | |
| Ser | Leu | Ala | Ala | Glu | Arg | Met | Leu | Trp | Arg | Asn | Arg | Phe | His | Lys | Thr | 340 | 345 | 350 | |
| Ser | Val | Gly | Met | Lys | Leu | Trp | Thr | Arg | Gln | Thr | Tyr | Lys | Tyr | Ile | Asp | 355 | 360 | 365 | |
| Asp | Ala | Glu | Ile | Glu | Val | Gln | Arg | Arg | Arg | Ser | Ala | Gly | Trp | Glu | Ala | 370 | 375 | 380 | |
| Glu | Leu | Arg | His | Arg | Ala | Tyr | Leu | Asn | Arg | Trp | Gln | Leu | Asp | Gly | Lys | 385 | 390 | 395 | 400 |

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro
 405 410 415

Glu Glu Asn Gly Gly Gly Thr Ile Pro Gly Thr Ser Arg Met Lys Ile
 420 425 430

Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Phe Met Leu Gly Lys Gln
 435 440 445

Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro
 450 455 460

Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg
 465 470 475 480

Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp
 485 490 495

Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu
 500 505 510

Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser
 515 520 525

Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys
 530 535 540

Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His
 545 550 555 560

Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu
 565 570 575

Asn Tyr Ser Phe
 580

(2) INFORMATION FOR SEQ ID NO: 38:

REPLACEMENT SHEET (RULE 26)

0020457-001404

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..1981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
 1 5 10 15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
 20 25 30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys
 35 40 45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
 50 55 60

Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser
 65 70 75 80

Ala Pro Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
 85 90 95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
 100 105 110

 09023457.081401
 104789.2549560

| | | | |
|---|-----|-----|-----|
| Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn | | | |
| 115 | 120 | 125 | |
| Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile | | | |
| 130 | 135 | 140 | |
| Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr | | | |
| 145 | 150 | 155 | 160 |
| Val Gly Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile | | | |
| | 165 | 170 | 175 |
| Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr | | | |
| | 180 | 185 | 190 |
| Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp | | | |
| | 195 | 200 | 205 |
| Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys | | | |
| | 210 | 215 | 220 |
| Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln | | | |
| 225 | 230 | 235 | 240 |
| Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys | | | |
| | 245 | 250 | 255 |
| Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr | | | |
| | 260 | 265 | 270 |
| Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala | | | |
| | 275 | 280 | 285 |
| Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn | | | |
| | 290 | 295 | 300 |
| Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly | | | |
| 305 | 310 | 315 | 320 |

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
325 330 335

Ala Ser Pro Thr Tyr Leu Ser Ile Glu Thr Thr Glu Lys Gly Ala Ala
340 345 350

Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly Leu Leu
355 360 365

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val
370 375 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385 390 395 400

Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys Gly Ser
405 410 415

Ala Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile
420 425 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Glu Leu
435 440 445

Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu Ser Asn
450 455 460

Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His
465 470 475 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser
485 490 495

Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln Leu Ala
500 505 510

00928457 "081401

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
 515 520 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
 530 535 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala
 545 550 555 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met
 565 570 575

Gly Val Glu Ala Gly Leu Leu Asn Val Thr Asn Thr Asn Leu Arg Thr
 580 585 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
 595 600 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
 610 615 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
 625 630 635 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
 645 650 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly
 660 665 670

Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile
 675 680 685

Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg
 690 695 700

Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn
 705 710 715 720

05928457.081401

Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn
725 730 735

Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser
740 745 750

Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn
755 760 765

Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln
770 775 780

Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn
785 790 795 800

Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr
805 810 815

Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val
820 825 830

Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu
835 840 845

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala
850 855 860

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
865 870 875 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
885 890 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala
900 905 910

0928457-081401
FOH T80 25482660

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser

915

920

925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys

930

935

940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr

945

950

955

960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln

965

970

975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr

980

985

990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn

995

1000

1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala

1010

1015

1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu

1025

1030

1035

1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala

1045

1050

1055

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu

1060

1065

1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys

1075

1080

1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly

1090

1095

1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg

1105

1110

1115

1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
 1125 1130 1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
 1140 1145 1150

Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys
 1155 1160 1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val
 1170 1175 1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu
 1185 1190 1195 1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val
 1205 1210 1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His
 1220 1225 1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly
 1235 1240 1245

Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val
 1250 1255 1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val
 1265 1270 1275 1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln
 1285 1290 1295

Ala Gly Val Gly Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys
 1300 1305 1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser
 1315 1320 1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu
 1330 1335 1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro
 1345 1350 1355 1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile
 1365 1370 1375

Glu Lys Leu Ser Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
 1380 1385 1390

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg
 1395 1400 1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile
 1410 1415 1420

Ala Leu Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val
 1425 1430 1435 1440

Leu Gly Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala
 1445 1450 1455

Ser Leu Ala Ser Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp
 1460 1465 1470

Val Gly Lys Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn
 1475 1480 1485

Leu Val Val Ala Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala
 1490 1495 1500

Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr
 1505 1510 1515 1520

Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val
 1525 1530 1535

Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala
 1540 1545 1550

Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu
 1555 1560 1565

Asp Gln His Tyr Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys
 1570 1575 1580

Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly
 1585 1590 1595 1600

Ala Ala Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn
 1605 1610 1615

Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser
 1620 1625 1630

Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn
 1635 1640 1645

Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser
 1650 1655 1660

Asp Lys Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys
 1665 1670 1675 1680

Gln Asn Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln
 1685 1690 1695

Asn Val Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp
 1700 1705 1710

| | | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|
| Ile | Lys | Thr | Val | Tyr | Asn | Pro | Lys | Lys | Phe | Ser | Asp | Asp | Lys | Ile | Leu |
| 1905 | | | | | 1910 | | | | | 1915 | | | | | 1920 |

REPLACEMENT SHEET (RULE 26)

Thr Lys Asp Thr Leu Leu Glu Cys Phe Lys Asn Ile Thr Thr Thr Gly
 35 40 45

His Phe Gly Val Ile Gly Ala Gln Tyr Glu Lys Ile Asp Ala Thr Arg
 50 55 60

Trp Ile Gly Asp Tyr Glu Glu Val Asn Gly Phe Glu Tyr Ile Asp Lys
 65 70 75 80

Ala Pro Ser Ile Tyr Phe Ser Val Gly Asp Asp Phe Asn Pro Glu Glu
 85 90 95

Leu Ile Ile Pro Ile Asn Leu Ala Tyr His Tyr Phe Asn Ile Ala Ile
 100 105 110

Ser Asp Phe Leu Ile Ala His Pro Glu Tyr Gln Lys Lys Cys Lys Glu
 115 120 125

Ile Gln Lys Thr Tyr Ser Gln Thr Asn Cys Ser Leu His Glu Thr
 130 135 140

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr
 1 5 10 15
 Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu
 20 25 30
 Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln
 35 40 45
 Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr
 50 55 60
 Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His
 65 70 75 80
 Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn
 85 90 95
 Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp
 100 105 110
 Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu
 115 120 125
 Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp
 130 135 140
 Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser
 145 150 155 160
 Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser
 165 170 175
 Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys
 180 185 190

REPLACEMENT SHEET (RULE 26)

Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu
405 410 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys
420 425 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val
435 440 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser
450 455 460

Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile
465 470 475 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser
485 490 495

Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr
500 505 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp
515 520 525

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala
530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val
545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys
565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile
580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val
595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg
610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr
625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp
645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp
660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg
675 680 685

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn
690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn
705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val
725 730 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr
740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu
755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser
770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu
785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr
 1 5 10 15

Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu
 20 25 30

Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln
 35 40 45

Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr
 50 55 60

Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His
 65 70 75 80

Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn
 85 90 95

Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp
100 105 110

Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu
115 120 125

Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp
130 135 140

Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser
145 150 155 160

Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser
165 170 175

Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys
180 185 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg
195 200 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu
210 215 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser
225 230 235 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu
245 250 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro
260 265 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile
275 280 285

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Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
 290 295 300

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys
 305 310 315 320

Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Val Val
 325 330 335

Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala
 340 345 350

Ala Ala Gly Thr Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala
 355 360 365

Ala Gly Thr Ala Ala Gly Thr Gly Val Ala Ala Gly Thr Ala Ala Thr
 370 375 380

Thr Gly Val Ala Ala Gly Thr Ser Ala Ala Ala Ile Thr Thr Ala Ala
 385 390 395 400

Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu
 405 410 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys
 420 425 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val
 435 440 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser
 450 455 460

Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile
 465 470 475 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser
 485 490 495

Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr
500 505 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp
515 520 525

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala
530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val
545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys
565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile
580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val
595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg
610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr
625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp
645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp
660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg
675 680 685

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Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn
 690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn
 705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val
 725 730 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr
 740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu
 755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser
 770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu
 785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Lys Lys Asp Ile Phe Tyr Cys Glu Gln Trp Ser Tyr Gly Tyr Lys
1 5 10 15

Arg Leu His Lys Pro Phe Ser Glu Lys Gln Ala Glu Glu Lys His Leu
 20 25 30

Lys Gly Glu Leu Tyr Thr Ala Val Ile Gly Ser Ala Thr Gln Pro Glu
 35 40 45

Tyr Val Ile Thr Leu Arg Glu Glu Val Gly Phe Phe Ser Val Asn Phe
 50 55 60

Phe Asp Lys Phe Gly Arg Asp Tyr Leu Thr His Gln Phe Gln Lys Tyr
65 70 75 80

Ser Asn Ser Asn Tyr Tyr Phe Leu Ser Met Ala Val Trp Arg Asp Tyr
 85 90 95

Ile Thr Leu Glu Ser His Asp Leu Ala Glu Gly Tyr Thr Tyr Phe Phe
 100 105 110

Asn Glu Asn Thr Asp Asp Cys Tyr Val Leu Lys Gln Asp Phe Ile Asn
 115 120 125

Asn Glu Arg Tyr Glu Lys Thr Glu Leu Tyr Ser Gln Lys Asp Lys Val
 130 135 140

Ile Leu Phe Pro Lys Phe Gly Glu Tyr Asp Leu Val Leu Asn Pro Asp
 145 150 155 160

Ile Ile

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Met Asn Lys Arg Met Lys Met Cys Pro Ala Cys Gln Gln Gly Tyr Leu
 1 5 10 15

Tyr His Ser Lys Pro Lys Tyr Leu His Asp Glu Ile Ile Leu Cys Asp
 20 25 30

Glu Cys Asp Ala Val Trp Leu Lys Gly Met Asn Ile Phe Tyr Gly Glu
 35 40 45

Tyr Glu Lys Asp Phe Tyr Ser Tyr Val Pro Phe Met Glu Ser Gln Gly
 50 55 60

Ile Thr Ser Glu Cys Ile Trp Glu Gly Asp Leu Phe Asp His Pro Tyr
 65 70 75 80

Tyr Glu Asp Glu Asn Ser Asn Asp Met Asp

85

90

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Ala Thr Glu Ile Glu Lys Ala Lys Ala Lys Ile Thr Ala Tyr
1 5 10 15

Ser Lys Leu Val Ala Gly Thr Ala Ser Ala Val Val Gly Gly Asp Val
20 25 30

Asn Thr Ala Ala Asn Ala Ala Gln Ile Ala Val Glu Asn Asn Thr Leu
35 40 45

Tyr Pro Arg Cys Val Gly Ala Lys Cys Asp Glu Phe Gln Lys Glu Gln
50 55 60

Gln Lys Trp Ile Arg Glu Asn Pro Glu Glu Tyr Arg Glu Val Leu Leu
65 70 75 80

Phe Gln Thr Gly Phe Ile Pro Ile Ile Gly Asp Ile Gln Ser Phe Val
85 90 95

Gln Ala Gln Thr Ala Ala Asp His Leu Phe Ala Leu Leu Gly Val Val
100 105 110

Pro Gly Ile Gly Glu Ser Ile Gln Ala Tyr Lys Val Ala Lys Ala Ala
115 120 125

Lys Asn Leu Gln Gly Met Lys Lys Ala Leu Asp Lys Ala Ala Thr Val
130 135 140

Ala Thr Ala Gln Gly Tyr Val Ser Lys Thr Lys Ile Lys Ile Gly Gln
145 150 155 160

Thr Glu Leu Arg Val Thr Ala Ala Thr Asp Lys Gln Leu Leu Lys Ala
165 170 175

Ile Gly Glu Gly Arg Asp Thr Thr Gly Lys Met Thr Glu Gln Leu Phe
180 185 190

Asp Ser Leu Ala Lys Gln Asn Gly Phe Arg Val Leu Ser Gly Gly Lys
195 200 205

Tyr Gly Gly Asn Asn Gly Phe Asp His Val Trp Gln Ala Ala Asp Gly
210 215 220

Ser Val Val Leu Ile Val Glu Ser Lys Gln Ile Arg Asn Gly Thr Val
225 230 235 240

Gln Leu Asn Pro Asn Gly Ala Gly Gly Tyr Thr Gln Met Ser Glu Asp
245 250 255

Trp Ile Arg Gln Val Leu Asp Gln Leu Pro Asp Gly Ser Pro Ala Lys
260 265 270

Ala Ala Val Phe Lys Ala Asn Lys Asn Gly Thr Leu Lys Thr Ala Ile
275 280 285

Ala Gly Val Asp Arg Gln Thr Gly Lys Ala Val Ile Leu Pro Val Lys
 290 295 300

Val Pro Ser Lys Thr Asn Ile Arg Arg
 305 310

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met Gly His Asn Met Met Thr Thr Gln Lys Trp Tyr Glu His Ile Thr
 1 5 10 15

Asn Val Ile Ile Gly Asn Thr Ala Asn Phe Asn Ser Gly Cys Leu Asp
 20 25 30

Ser Ile Asp Tyr Val Asp Glu Arg Lys Gly Val Pro Leu Ala Ala Met
 35 40 45

Gln His Ile Phe Met Asp Val Arg Ala Ala Ala Ser His Ala Tyr Leu
 50 55 60

Phe Glu His Asp Leu Lys Lys Phe Lys Gln Tyr Ala Tyr Val Ala Gly
65 70 75 80

Lys Leu Gly Val Leu Leu Ser Val Asn Ser Thr Asp Pro Glu Pro Phe
85 90 95

Phe Phe Pro Cys Asp Met Leu Asn Ile Gln Asn Pro Met Phe Leu Met
100 105 110

Leu Met Ser Asp Ser Pro Gln Leu Arg Glu Phe Leu Val Arg Asn Ile
115 120 125

Asp Asn Ile Ala Asn Asp Thr Glu Ala Phe Ile Asn Arg Tyr Asp Leu
130 135 140

Asn Arg His Met Ile Tyr Asn Thr Leu Leu Met Val Glu Gly Lys Gln
145 150 155 160

Leu Asp Arg Leu Lys Gln Arg Ser Glu Lys Val Leu Ala His Pro Thr
165 170 175

Pro Ser Lys Trp Leu Gln Lys Arg Leu Tyr Asp Tyr Arg Phe Phe Leu
180 185 190

Ala Phe Ala Glu Gln Asp Ala Glu Ala Met Lys Ala Ala Leu Glu Pro
195 200 205

Leu Phe Asp Lys Lys Thr Ala Arg Met Ala Ala Lys Glu Thr Leu Ser
210 215 220

Tyr Phe Asp Phe Tyr Leu Gln Pro Gln Ile Val Thr Tyr Ala Lys Ile
225 230 235 240

Ala Ser Met His Gly Phe Asp Leu Gly Ile Asp Gln Glu Ile Ser Pro
245 250 255

Arg Asp Leu Ile Val Tyr Asp Pro Leu Pro Ala Asp Glu Tyr Gln Asp
260 265 270

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Ile Phe Asp Phe Met Lys Gln Tyr Asp Leu Ser Tyr Pro Tyr Glu Tyr
 275 280 285

Leu Gln Asp Trp Ile Asp Tyr Tyr Thr Phe Lys Thr Asp Lys Leu Val
 290 295 300

Phe Gly Asn Ala Lys Arg Glu
 305 310

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCCACCGGTA CGGAAACTGA A

21

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTGAATTCA TGTCTATTCC ATTTTGAAGA

30

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CCGAGATCTT TAACCCTTTG GGCTTAAGCG A

31

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGGAGATCTC CCGCTCGTGT TGTGCATTA

29

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AAGAGATCTG CAGCCAAGGC TCTCGAAA

28

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GGGAGATCTC AGGCTGCCGC CGTTGA

26

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGGAGATCTC ACCCCAAGAA CGCCAAAA

28

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGGAGATCTG AACGTATAGT AATCTATCCA A

31

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AGTGGCTCCT AG

12

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(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

AGCACTCTCC AGCCTCTCAC CGAG

24

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGTGGCTCTT AA

12

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

AGTGGCTGGC

10

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGCACTCTCC AGCCTCTCAC CGAC

24

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTACTTGCCT AG

12

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACCGACGTCG ACTATCCATG AACG

24

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTACTTGCTT AA

12

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTACTTGGGC

10

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGACGTCG ACTATCCATG AACC

24

(2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCTCCCT CG

(2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGGCAACTGT GCTATCCGAG GGAG

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GATCAACTTT TCCCTGTTTG TCCATTACC GGTTTGAATG AACCGATTGC GCGCCGCGCG 60

TGTTGTTGGA CATTACCTGC GATTCAGACG GTACGATTGA CCACTACATC GAGGAGAACG 120

GCAATCAGGG TACAATGCTA 140

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

| | |
|---|-----|
| GATCCGCGTA CTTGGTTTTT CATATTTTGC ATAGTCTTGT CGGTCGGGCA TCTTCCCCGA | 60 |
| CATCATCTAA ATTTGTCTTT ATTGGTTTTT ACGCCACTCA TTGCGGATAA ACAATATTCC | 120 |
| GCCTTGCCGT CGCGAATGTT CAAGCTAGCC TGCATCACCG TAATCAGGTT GCCCGTTACC | 180 |
| GAGCCTTCGA GA | 192 |

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

| | |
|---|-----|
| GATCCGGCTG CCCGACGCGC GCAAAATTGC CGCCGAGGAA AGCGCGCACA ACCACGACGG | 60 |
| CAAAACCAGC GTATGGCAAT ACAAACATCT CGTGTTCGGT ACGGCAGGCA TTTTCTGCTA | 120 |
| TGTCGGCGCG GAGGTGTCTA TCGGTTCGTT GATGGTCAAC GTATTGGGTT ATCTGAAAGG | 180 |
| GCTGGATC | 188 |

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GATCCCCCAC TTTACCTCGG GCAGATTTTG CGCGTTCATT ACAATAGCGT ATTTATGCGT 60

TTGCGTTTGC GCTTGCCGCT GCGCGGATATG GGAAAACATC AATATGGCGG 120

TATAAAGCGC GGTATGGCGG AAAACCTGCC GTTCCAAGT TTTATTCATC TTTTATTCCT 180

TGAGTTTGCC TTCACGGGAC GGGGCGGCGC GCGGAACGCG GGGTTCGGTA AACCGCCCGA 240

TTCCGCGCCC GCCGAATTGC TGATTGAAAA GCTTACTTCC CCATTTTAAC TTTGCACACT 300

GATC 304

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

| | |
|---|-----|
| GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC | 60 |
| GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT | 120 |
| CAGGAAAACG GTCGGAATGC CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG | 180 |
| CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG | 240 |
| ATC | 243 |

(2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGGCGGCGTAGTccgccGcgACAGCGTTACCATAAGCGGGACAGACTACACCCCTTTATCTAACCCGC
 AAAGTTTGGATACGGAATTAAAATGGTTGCTTCAAGAAGCTCCCGAAATAGAAAATCCTTTTCGACCGC
 GCCGTTTATCTCCATAATAATTTGGCGTATCTTCAATATTTTAAAGATTGCAATAAACGTACTGCCAG
 AAAGTGCATGACCTTGTCGCTGATGCGCTCCG

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGGTCAATCA CAAGAAAGTC AGCCGTCTGA TGGCGAAGAC GGGGCTGAAG GCAGTGATAT 60

GGCGGCGCAA ATACCGCTCG TTCAAAGGAG AAGTCGGCAA AATTGCGCCG AATATCCTGC 120

GACGCTGTTT CCATGCAGAA AAGCCGAATG AGAAATGGGT AACGGACGTT GCCGAGTTCA 180

ATGTAGGCGG AGAAAAGATA TACCTTTCTC CGATTATGGA TTTGTTTAAC GGGGAAATCG 240

TCAGTTACCG TATTCAGACC CGCCCGACTT TCGATTGTC 280

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

CGGTGTTTTT CTTAACAATT CGCCGACTTC ATGGCGATAT TTAAGTGACA GTTGCTCCGC      60
CCACGCAGTT GCGCCGAAC CAGCACCACG ACATTATACT GATTATGCAC ATCGGCAAGA      120
TCAAAGTGAC CTATCGTAGT ATCGCAGACT GT                                     152

```

(2) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

CGGGAGGTTTTGTGCATCCTGATACCGATCGGTTGTTGTTGCTCAAAGGACAGAAGGCCGCTGATAAA
CGAGATTACCTGTTTGTGCTATTGACGATTTTATACTCTGCCATTTTGCCAGACAAAACCGCAGAC
AGTGCTGCCAAGTTTCTGACCGAACATCTGGCCGACCCCTGCTTGACCTGATTGAGTACGCTTACTC
TGACAATGATAGGTAATATAAAGAGCCGTCCAACATGCTTTCGGTGACGTTTGTTATGATAATGGGAT
TGTTTGGAGGCTTGCCCGATTTGCTTGTCCTGCGCAGACCAACGGTAAGGCGGAGCGGGTTATCCGTACCT
TGATGGAGATGTGGCATGAGGAACAGTCGTTTGACAGACCG

```

(2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG 60

ATTTTTATTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA 120

GAATTCCAAC GGGTAAAAAA GGCCTTGTA AATTGGCATT ATTCTGGCTT GGCAACAAAA 180

TTGAAATTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA 240

TTCGAAGAAG CAAGGGTATT TATCAACCG 269

(2) INFORMATION FOR SEQ ID NO: 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CGGATGAAAACGGGCATACGCgcCAAAGTATTTACGAACATCAaAGGCTTGAAGATACCGCACACCTAC
ATAGAAACGGACGCGAAAAAGCTGCCGAAATCGACAGATGAGCAGCTTTCTGGCGCATGATATGTACGA
ATGGATAAAGAAGCCCGAAAAATATCGGGTCTATTGTCATTGTAGATGAAGCTCAAGACGTATGGCCG

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

| | |
|---|-----|
| CGGTTTCAGG TTGTCGCGAA GGCTCGGTAA CGGGCAACCT GATTACGGGT GATGCAGGCA | 60 |
| GCTTGAACAT TCGCGACGGC AAGGCGGAAT ATGTTTATCC GCAATGAGTG GCGTAAAAAC | 120 |
| CAATAAAGAC AAATTTAGAT GATGTCGGGG AAGATGCCCC ACCGACAAGA CTATGCAAAA | 180 |
| TATGAAAAAC CAAGTACGCG GATCAGGCAT GGATGCACGA TCCAATCCG | 229 |

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

| | |
|---|-----|
| CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAAATA | 60 |
| TTGTGTATCG GGGGGGGGTA TTTGCTGACG TAAAAACTA TAAACGCCGC GCAAAATATG | 120 |
| GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG ATGGATAAAA TCGCCAGCGA | 180 |
| TAAAGAATTT GCGAGAACCT GATGCCG | 207 |

(2) INFORMATION FOR SEQ ID NO: 81 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

| | |
|---|-----|
| CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT | 60 |
| TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC | 120 |
| TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA | 180 |

AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG

224

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

| | |
|---|-----|
| CGGGAACAGC CATTGCCCAC GCCCACGCCC CCCAAGAAAG ACGGAAACTA CTGCCTAAAT | 60 |
| TTTCGGCAAT CAAGTTGACG ATTAAAGGGT TGGGGGCAGT TGCAGTAATA AACATAGCCG | 120 |
| ACGAAATGGG ATTGGAATGA TAGTTGACCA AAGCCAAATA TTTACCCATC TTGCCTTCTG | 180 |
| TGCCTTTTGC GGGATTGGAG CCGTAACTGC CG | 212 |

(2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

| | |
|---|-----|
| CGGGAATTCT GAGCAGAATG AAAGAAAGCA GGCTTGATAA TTTCATAAAG TTATTGGAAG | 60 |
| AAAAAGGATT TACCGTCCAT TTCGGTATTC ACAATACGGC TGATTACGGA ATTCCCCAAA | 120 |
| GCCGTAAAAG ATTTACGTTA ATTGCAAACA GAATAACCAA AGAAAAGCTG GAACCAGTCA | 180 |
| AGTATTCGGG CAAACGGCTT ACGGTAGCCG ATGTTTTGGG AATGGAAATG GCTTTCCCAA | 240 |
| CATTATTGCA GGACACCAAG ACGAAACGGA TTTTATGCAT AGCTGTGCGG GAATTATCTG | 300 |
| ATATCACTTG AACGATTGGC TTGATACCTA AAAACGGAGG AACCGTTGGC TTT | 353 |

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

| | |
|---|-----|
| AATTCCGTAT CCAAACCTTG CGGGTTAGAT AAAGGGGTGT AGTCTGTCCC GCTTATGGTA | 60 |
| ACGCTGTGCG GGCGGACTAC GCGCGGAGCC TTTTCCAGT AAGTTTTCGG AAATCAGGCT | 120 |
| GTGGGTGGTT TTTAAGAAAT CCAACCAGTC AAACGGCTCG GGGCTGTCCA AACCGGACAC | 180 |

AGGTGCCGGT AACTTTCCCT CAGGTTGATT AACATTACGG CATCCGAATA TAACTTCCCG 240
 CCTGCGGTTT GCCCGAGTTT AAGCAATGCC TCGTATCGT ATTGATTATA AAGTGTTC 300
 TTCCAATT 308

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AATTCGTGTG CCGCGTCGAC AAACCGCTGA CGTAGCGGAT GTTCATGCC ACGTTTCAAA 60
 GCAGGTTGAT GGCGGTTAGC AACCTCTGA TTCACTGGG ATAT 104

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AAATTGCGTAG AGTGGGCTTC AGCCACGTTT TTTCTTTTTC GGTCGTTGAT TGGTGGGCTG 60

AACCACTTGT TTCGGAAATC CGTATCATG 89

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC 60

AAAAGCGCGG GGTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA 120

AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT 180

TGCACACGTT TGGATAAGGA TGC GCGGCGG TTT CAGTATC AA ACTGAAAA AATATCCTGC 240

TATGTTTCCA TCAATCGCGC AAACCGATAA ATT 273

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

| | |
|--|-----|
| AATTCTTCCG CACGGGGAGG CTTGTTTTTC TTCCCTTCTG TTCCGACCGA TTCTCAAATA | 60 |
| AAAATCATTG ATTTTCATCGA AGTTCATTCC TATACCATTA TCTTTAATAA CGATTTTATG | 120 |
| CTCCGGTTTA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTTCG | 180 |
| TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTTCGA | 240 |
| TTACGGTTGG CTCGAAACTC AATTTC AATT | 270 |

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AATTATGAAC ACACGCATCA TCGTTTCGGC TCGTTTCGTT GCGTTGGCAT TAGCAGGTTG 60
 CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAACTT CAGGAACGTG CCGCGTTTGC 120
 CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA 180
 CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCAGTGT AATCAGCACA 240
 ATCGGCGTTA CCACTTCCGA TGCAATT 267

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AATTTTTATT TGGTTCGTAG TCATTTTGTG CAACTGAACG ATATTCGTTT TCATCATTGC 60
 TAACGTCTAG TGCCCATTGT GGCCCGTAAT AAGAGATTTC GTCTCCTTTT ACATGTTTGA 120
 CGCTGACGGC ATACTGGGGA TCGATGACGG ATAATGTACG TCTGTTGACA TCTGCAACGC 180
 TAAATCAATC ATCGGTATTG GATAATGCGT TGCCGATGTT TTGACTTGTA TGTT 234

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

| | |
|--|-----|
| AATTCGGCCG GCTGTGTCAA ATAATGCGTT ACTTTGGCCG GGTCTTGTTT TTTGTAAGTG | 60 |
| GTGGTCTTTT TTTGCGCGTT ATCCCCATCT GTTTGAGTGC ATAGCAAATG GTGGCTGCCG | 120 |
| TACAATCAAA TGTTTGGCGT TCATGCAGAT AGGCATCATG GTGTTGCCCA ATATATTGAG | 180 |
| CCGGTTTTTTG CCTATCCGAT TTGACGGCAT TTAGACCGGT AACTTGATGT TTTAAGCTGC | 240 |
| CTGTTTGTTT AAAGGCGAAT CCACAAGTAA AGCGTGTTTC TTGACAGGTT AAACG | 295 |

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AATTGTGTAT ATCAAGTAGG ATGGGCATTT ATGCCTGACC TACAAAACCA AAAACAACCT 60
 ACCACCCTTA ATCAACTCCA CAAACCCTCT TCAGACAACC TCGTTTTTTTG AAAACAATC 120
 TGTAAACAGA TAACTGCTGA AGAATACCGT TGCCGAGCCC CAAAACCCGT ACTGCAACTT 180
 TTATTGTGAA CTTCCCATTA TGAGAAAATC CCTTTTCGTC CTCTTTCTGT ATTCGTCCCT 240
 ACTTACTGCC AGCGAAATT 259

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AATTGCACCA CGCGATGATG GGTACGCCTC TGTTGCCATT GCGACCGCCG CCGCCGTGCC 60
 CGGTACGCTG GTCAACCTTG CCGCGGCGGA ACGGGTAAAG AAGTGCGCTT CGGGCATCCT 120
 TCCGGTACAT TGC GCGTCGG TGCAGCGCCG AATGTCAGGA CGGACAATGG ACGGCCACCA 180
 AAGCGGTTAT GAGCCGCAGC GCACGCGTGA TGATGGAAGG TTGGGTCAGG GTGCCGGAAG 240
 ATTGTTTTTA AATTGGACGG CGAACCGGTC TATTCGTATT GCGGTTATAC CGCCGCAAAG 300
 GCAGACCTTG AAACCTGGTGC GTGCCGTGCA GGGCATGTAC GGCTATGTGT GCGTGCGGGG 360

CGGATTTGAT GTGCGGAAT

379

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

| | |
|---|-----|
| AATTTGTTGG GCAGATGGCC GTGAATCAGC AGGTGGGCGA CTTCTTCAAA CTCGCATTTT | 60 |
| TGTGCCAAAT CCAGAATGTC GTAACCGCGA TACGTCAAAT CGTTGCCGGT ACGCAACGGT | 120 |
| ACACAAAGCG GTATTACCGG CCGCAACGCC AGAAAGCGCA ACGGATTTTT AGGTTTGAGG | 180 |
| GTCGGGGTTT GAGTAGTTTC AGTCATGGTA TTTCTCCTTT GTGTTTTTAT GGGTTTCGGG | 240 |
| TTTTCAGACG ACCGATGCGG ATTTGTTGAA AGGCAGTCTG AAAGCGGTAA ATCATTTTTG | 300 |
| AAACAATT | 308 |

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

| | |
|---|-----|
| AATTCGGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGGCGGTGA TAAAACAGAC | 60 |
| GAGGGTATCC GCCTGATGCA ACAGAGCGAT TACGGCAACT TGTCTACCA CATCCGTAAT | 120 |
| AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAACT | 180 |
| GACCTATTG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT | 240 |
| AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTGC GGAATT | 286 |

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

| | |
|---|-----|
| AATTTGGATA CGTTGGAAAA GGGATATTTG ATTGGGAATG GGATGAAGAT AAGCGTAGAT | 60 |
| GAGTTGGGGA AAAAAGTGTT AGAACATATC GGTAAGAATG AACCGTTATT GTTGAAAAAT | 120 |

CTACTGGTTA ACTTCAATCA GGGAAAACAT GAAGAAGTTA GGAAGTTGAT TTATCAGTTG 180
 ATAGAGTTAG ATTTTCTGGA ACTTTTGTGA GGGATTCTAT GAAAAACTGG AAGCAATT 238

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AATTCGGCAC GCAGGTTTTT TAAAAAAGG CCGTTGATGA CTTTGTGAT ATTGGCGGCT 60
 TCGGTGTAGT GCGCGCCCGC TTCGGCCGCT CTTGCGCGTC CATGACGGAT TGGAAGAGCG 120
 TGCCGAAGAT TTCTGGACTG ATGTTGCGCC AGTCGAAATT GCCGACACGG GAGGAATACC 180
 TGCCAACAAG AGTGCAGGCA GCGTAATCAA ACCACCCCCA CCCGCAATCG CATCGATAAA 240
 TCCGGCAATC ATCGCAACCA AACCCAAAGC GAGTATTATG TATAAATCTT CCATGTTTCT 300
 TAATCCTGTT AACTGCACC AA 322

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

| | |
|--|-----|
| AATTTGTCGG CAATCTTCCC GGGTCGCTTT ATTTTGTGCA GGCATTATTT TTCATTTTGTG | 60 |
| GCTTGACAGT TTGGAGATAT TGTGTATCGG GGGGGGGTAT TTGCTGACGT AAAAAACTAT | 120 |
| AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG | 180 |
| ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG ATGCCGGCCT GTTGTTGAAT | 240 |
| ATTTTCGACC TGTAATTACG ATTTGGCTTC CGCGCCGGCA CAATATGCCG CCAAGCGGCG | 300 |
| CCCACATTTT GGAAGC | 316 |

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

| | |
|---|-----|
| AATTCGGACA GTATGAATAC AGCGGATTAA TACAAGGTAA GTTCATTACA ACGGAAAAAC | 60 |
| CTTTAAAGAA TAATATGAAA GGTATTACCT TGTTTGCCAA CGGGAATGGT AAATATGCCC | 120 |
| GAGTTTTTCA CTGAATAGCG AATCCAGCCA TTTCTATTCA TATTGACTG GATGGCTGAA | 180 |
| TGTGGACTTT ATAGATAATG ACGATGAAGA TTTAATT | 217 |

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